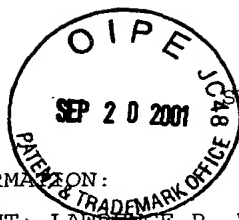


3



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LAWRENCE P. WACKETT
- (ii) TITLE OF INVENTION: DNA MOLECULES AND PROTEIN DISPLAYING
IMPROVED TRIAZINE COMPOUND DEGRADING ABILITY
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
 - (B) STREET: 119 North Fourth Street
 - (C) CITY: Minneapolis
 - (D) STATE: Minnesota
 - (E) COUNTRY: USA
 - (F) ZIP: 55401
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30¹²⁸
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/866,307
 - (B) FILING DATE: 25-MAY-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/035,404
 - (B) FILING DATE: 17-JAN-1997
 - (A) APPLICATION NUMBER: PCT/US98/00944
 - (B) FILING DATE: 16-JAN-1998
 - (A) APPLICATION NUMBER: 09/155,036
 - (B) FILING DATE: 17-SEPT-1998
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: PROVENCE, DAVID L.
 - (B) REGISTRATION NUMBER: 43,022
 - (C) REFERENCE/DOCKET NUMBER: 110.00440102
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-305-1005
 - (B) TELEFAX: 612-305-1228

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC TTCTTGAGCG CGGCCACAGC AGCCTTGATC ATGAAGGCCGA GCATGGTGAC	60
CTTGACGCCG CTCTTTTCGT TCTCTTTGTT GAACTGCACG CGAAAGGCTT CCAGGTCGGT	120
GATGTCCGCG TCGTCGTGGT TGGTGACGTG CGGGATGACC ACCCAGTTGC GGTGCAGGTT	180
TTTCGATGGC ATAATATCTG CGTTGCGACG TGTAACACAC TATTGGAGAC ATATCATGCA	240
AACGCTCAGC ATCCAGCACG GTACCCTCGT CACGATGGAT CAGTACCGCA GAGTCCTTGG	300
GGATAGCTGG GTTCACGTGC AGGATGGACG GATCGTCGCG CTCGGAGTGC ACGCCGAGTC	360
GGTGCCCTCCG CCAGCGGATC GGGTGATCGA TGCACGCGGC AAGGTCGTGT TACCCGGTTT	420
CATCAATGCC CACACCCATG TGAACCAGAT CCTCCTGCGC GGAGGGCCCT CGCACGGACG	480
TCAATTCTAT GACTGGCTGT TCAACGTTGT GTATCCGGGA CAAAAGGCCGA TGAGACCGGA	540
GGACGTAGCG GTGGCGGTGA GGTGTATTG TGCGGAAGCT GTGCGCAGCG GGATTACGAC	600
GATCAACGAA AACGCCGATT CGGCCATCTA CCCAGGCAAC ATCGAGGCCG CGATGGCGGT	660
CTATGGTGAG GTGGGTGTGA GGGTCGTCTA CGCCCGCATG TTCTTTGATC GGATGGACGG	720
GCGCATTCAA GGGTATGTGG ACGCCTTGAA GGCTCGCTCT CCCCAAGTCG AACTGTGCTC	780
GATCATGGAG GAAACGGCTG TGGCCAAAGA TCGGATCACA GCCCTGTCAG ATCAGTATCA	840
TGGCACGGCA GGAGGTCGTA TATCAGTTTG GCCCCGCTCCT GCCACTACCA CGGCGGTGAC	900
AGTTGAAGGA ATGCGATGGG CACAAGCCTT CGCCCGTGAT CGGGCGGTAA TGTGGACGCT	960
TCACATGGCG GAGAGCGATC ATGATGAGCG GATTCATGGG ATGAGTCCCG CCGAGTACAT	1020
GGAGTGTTAC GGACTCTTGG ATGAGCGTCT GCAGGTCGCG CATTGCGTGT ACTTTGACCG	1080
GAAGGATGTT CGGCTGCTGC ACCGCCACAA TGTGAAGGTC GCGTCGCAGG TTGTGAGCAA	1140
TGCCTACCTC GGCTCAGGGG TGGCCCCCGT GCCAGAGATG GTGGAGCGCG GCATGGCCGT	1200
GGGCATTGGA ACAGATAACG GGAATAGTAA TGA CTCCGCA AACATGATCG GAGACATGAA	1260
GTTTATGGCC CATATTCACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA	1320
GATTCTTGAA ATGGCGACGA TCGATGGGGC GCGTTTCGTTG GGAATGGACC ACGAGATTGG	1380
TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG	1440

ACTCTCACAT CATTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC 1500
 TGTCTGATT GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA 1560
 ACGTGAGTTG GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC 1620
 GAACATGGTG GCTAACCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC 1680
 GCCGCCCTT GAGGAAATCG CTGCCATCTT GCGCGGCTC GGATTGGGGG GCGGACATGA 1740
 CCTTGATGGA TACAGAATTG CCATGAATGC GGCACCTCCG TCCTTCGCTC GTGTGGAATC 1800
 GTTGGTAGGT GAGGGTCGAC TCGGGCGCC AGCTTCCCGA AGAGGTGAAA GGCCCGAG 1858

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln
1				5					10					15	
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg
			20					25					30		
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp
			35				40					45			
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn
	50					55					60				
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His
65					70					75				80	
Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	Gly	Gln
			85						90					95	
Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys
			100					105					110		
Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp
			115				120					125			

Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140
 Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160
 Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175
 Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190
 Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205
 Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220
 Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240
 Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255
 Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270
 Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285
 His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300
 Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320
 Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Ala Asn
 325 330 335
 Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350
 Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
 355 360 365
 Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
 370 375 380
 Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Leu
 385 390 395 400
 Arg Arg Leu Ser His His Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr
 405 410 415
 Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met Glu
 420 425 430
 Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu
 435 440 445

Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn Met
 450 455 460

Val Ala Asn Pro Ala Trp Arg Ser Leu
 465 470

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGAGCATGG TGACCTTGAC GCCGCTCTTT TCGTTCTCTT TGTTGAACTG CACGCGAAAG	60
GCTTCCAGGT CGGTGATGTC CGCGTCGTCG TGGTTGGTGA CGTGCGGGAT GACCACCCAG	120
TTGCGGTGCA GGTTTTTCGA TGGCATAATA TCTGCGTTGC GACGTGTAAC AACTATTTGG	180
AGACATATCA TGCAAACGCT CAGCATCCAG CACGGTACCC TCGTCACGAT GGATCAGTAC	240
CGCAGAGTCC TTGGGGATAG CTGGGTTTAC GTGCAGGATG GACGGATCGT CGCGCTCGGA	300
GTGCACGCCG AGTCGGTGCC TCCGCCAGCG GATCGGGTGA TCGATGCACG CGGCAAGGTC	360
GTGTTACCCG GTTTCATCAA TGCCACACC CATGTGAACC AGATCCTCCT GCGCGGAGGG	420
CCCTCGCACG GCGTCAATT CTATGACTGG CTGTTCAACG TTGTGTATCC GGGACAAAAG	480
GCGATGAGAC CGGAGGACGT AGCGGTGGCG GTGAGGTTGT ATTGTGCGGA AGCTGTGCGC	540
AGCGGGATTA CGACGATCAA CGAAAACGCC GATTCGGCCA TCTACCCAGG CAACATCGAG	600
GCCGCGATGG CGGTCTATGG TGAGGTGGGT GTGAGGGTCG TCTACGCCCG CATGTTCTTT	660
GATCGGATGG ACGGGCGCAT TCAAGGTAT GTGGACGCCT TGAAGGCTCG CTCTCCCCAA	720
GTGGAAGTGT GCTCGATCAT GGAGGGAACG GCTGTGGCCA AAGATCGGAT CACAGCCCTG	780
TCAGATCAGT ATCATGGCAC GGCAGGAGGT CGTATATCAG TTTGGCCCGC TCCTGCCACT	840
ACCACGGCGG TGACAGTTGA AGGAATGCGA TGGGCACAAG CCTTCGCCCG TGATCGGGCG	900
GTAATGTGGA CGCTTCACAT GCGGAGAGC GATCATGATG AGCGGATTCA TGGGATGAGT	960
CCCGCCGAGT ACATGGAGTG TTACGGACTC TTGGATGAGC GTCTGCAGGT CGCGCATTCG	1020
GTGTACTTTG ACCGGAAGGA TGTTCGGCTG CTGCACCGCC ACAATGTGAA GGTCGCGTCG	1080
CAGGTTGTGA GCAATGCCTA CCTCGGCTCA GGGGTGGCCC CCGTGCCAGA GATGGTGGAG	1140
CGCGGCATGG CCGTGGGCAT TGGAACAGAT AACGGGAATA GTAATGACTC CGTAAACATG	1200



ATCGGAGACA TGAAGTTTAT GGCCCATATT CACCGCGCGG TGCATCGGGA TGCGGACGTG	1260
CTGACCCCAG AGAAGATTCT TGAAATGGCG ACGATCGATG GGGCGCGTTC GTTGGGAATG	1320
GACCACGAGA TTGGTTCCAT CGAAACCGGC AAGCGCGCGG ACCTTATCCT GCTTGACCTG	1380
CGTCACCCTC AGACGACTCC TCACCATCAT TTGGCGGCCA CGATCGTGTT TCAGGCTTAC	1440
GGCAATGAGG TGGACACTGT CCTGATTGAC GGAAACGTTG TGATGGAGAA CCGCCGCTTG	1500
AGCTTTCTTC CCCCTGAACG TGAGTTGGCG TTCCTTGAGG AAGCGCAGAG CCGCGCCACA	1560
GCTATTTTGC AGCGGGCGAA CATGGTGGCT AACCCAGCTT GGCGCAGCCT C'TAGGAAATG	1620
ACGCCGTTGC TGCATCCGCC GCCCCTTGAG GAAATCGCTG CCATCTTGGC GCGGCTCGGA	1680
TTGGGGGGCG GACATGACCT TGATGGATAC AGAATTGCCA TGAATGCGGC ACTTCCGTCC	1740
TTCGCTCGTG TGGAATCGTT GGTAGGTGAG GGTGCGACTGC GGGCGCCAGC TTCCCGAAGA	1800
AGTGAAAG	1808

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAGCGCCGCC ACAGCAGCCT TGATCATGAA GGCGAGCATG GTGACCTTGA CGCCGCTCTT	60
TTCTGTTCTCT TTGTTGAACT GCACGCGAAA GGCTTCCAGG TCGGTGATGT CCGCGTCGTC	120
GTGGTTGGTG ACGTGCGGGA TGACCACCCA GTTGCGGTGC AGGTTTTTCG ATGGCGTAAT	180
ATCTGCGTTG CGACGTGTAA CACACTATTG GAGACATATC ATGCAAACGC TCAGCATCCA	240
GCACGGTACC CTCGTCACGA TGGATCAGTA CCGCAGAGTC CTTGGGGATA GCTGGGTTCA	300
CGTGCAGGAT GGACGGATCG TCGCGCTCGG AGTGCACGCC GAGTCGGTGC CTCCGCCAGC	360
GGATCGGGTG ATCGATGCAC GCGGCAAGGT CGTGTTACCC GGTTTCATCA ATGCCACAC	420
CCATGTGAAC CAGATCCTCC TGC GCGGAGG GCCCTCGCAC GGGCGTCAAT TCTATGACTG	480
GCTGTTCAAC GTTGTGTATC CGGGACAAAA GGCGATGAGA CCGGAGGACG TAGCGGTGGC	540
GGTGAGGTTG TATTGTGCGG AAGCTGTGCG CAGCGGGATT ACGACGATCA ACGAAAACGC	600
CGATTGCGCC ATCTACCCAG GCAACATCGA GGCCGCGATG GCGGTCTATG GTGAGGTGGG	660
TGTGAGGGTC GTCTACGCC GCATGTTCTT TGATCGGATG GACGGGCGCA TTCAAGGGTA	720

TGTGGACGCC TTGAAGGCTC GCTCTCCCCA AGTCGAACTG TGCTCGATCA TGGAGGAAAC 780
 GGCTGTGGCC AAAGATCGGA TCACAGCCCT GTCAGATCAG TATCATGGCA CGGCAGGAGG 840
 TCGTATATCA GTTTGGCCCG CTCCTGCCAC TACCACGGCG GTGACAGTTG AAGGAATGCG 900
 ATGGGCACAA GCCTTCGCCC GTGATCGGGC GGTAATGTGG ACGCTTCACA TGGCGGAGAG 960
 CGATCATGAT GAGCGGATTC ATGGGATGAG TCCC GCCGAT TACATGGAGT GTTACGGACT 1020
 CTTGGATGAG CGTCTGCAGG TCGCGCATTG CGTGTACTTT GACCGGAAGG ATGTTCTGGCT 1080
 GCTGCACCGC CACAATGTGA AGGTGCGGTC GCAGGTTGTG AGCAATGCCT ACCTCGGCTC 1140
 AGGGGTGGCC CCCGTGCCAG AGATGGTGGG GCGCGGCATG GCCGTGGGCA TTGGAACAGA 1200
 TAACGGGAAT AGTAATGACT CCGTAAACAT GATCGGAGAC ATGAAGTTTA TGGCCCATAT 1260
 TCACGCGCGG GTGCATCGGG ATGCGGACGT GCTGACCCCA GAGAAGATTC TTGAAATGGC 1320
 GACGATCGAT GGGGCGCGTT CGTTGGGGAT GGACCACGAG ATTGGTTCCA TCGAAACCGG 1380
 CAAGCGCGCG GACCTTATCC TGCTTGACCT GCGTCACCCT CAGACGACTC CTCACCATCA 1440
 TTTGGCGGCC ACGATCGTGT TTCAGGCTTA CGGCAATGAG GTGGACACTG TCCTGATTGA 1500
 CGGAAACGTT GTGATGGAGA ACCGCCGCTT GAGCTTTCTT CCCCTGAAC GTGAGTTGGC 1560
 GTTCCTTGAG GAAGCGCAGA GCCGCGCCAC AGCTATTTTG CAGCGGGCGA ACATGGTGGC 1620
 TAACCCAGCT TGGCGCAGCC TCTAGGAAAT GACGCCGTTG CTGCATCCGC CGCCCCCTGA 1680
 GGAAATCGCT GCCATCTTGG CGCGGCTCGG ATTGGGGGGC GGACATGACC TTGATGGATA 1740
 CAGAATTGCC ATGAATGCGG CACTTCCGTC CTTGCTCGT GTGGAATCGT TGGTAGGTGA 1800
 GGGTCGACTG CGGGCGCCAG CTTCCCGAAG AAGTGAAAGG CCCGAG 1846

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Ser Met Val Thr Leu Thr Pro Leu Phe Ser Phe Ser Leu Leu Asn
 1 5 10 15
 Cys Thr Arg Lys Ala Ser Arg Ser Val Met Ser Ala Ser Ser Trp Leu
 20 25 30
 Val Thr Cys Gly Met Thr Thr Gln Leu Arg Cys Arg Phe Phe Asp Gly
 35 40 45

Ile Ile Ser Ala Leu Arg Arg Val Thr His Tyr Trp Arg His Ile Met
 50 55 60
 Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln Tyr
 65 70 75 80
 Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg Ile
 85 90 95
 Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp Arg
 100 105 110
 Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn Ala
 115 120 125
 His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His Gly
 130 135 140
 Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln Lys
 145 150 155 160
 Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys Ala
 165 170 175
 Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp Ser
 180 185 190
 Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly Glu
 195 200 205
 Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met Asp
 210 215 220
 Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro Gln
 225 230 235 240
 Val Glu Leu Cys Ser Ile Met Glu Gly Thr Ala Val Ala Lys Asp Arg
 245 250 255
 Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg Ile
 260 265 270
 Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu Gly
 275 280 285
 Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp Thr
 290 295 300
 Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met Ser
 305 310 315 320
 Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu Gln
 325 330 335
 Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu His
 340 345 350
 Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr Leu
 355 360 365
 Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met Ala

Thr Pro Leu Phe Ser Phe Ser Leu Leu Asn Cys Thr Arg Lys Ala Ser
 20 25 30
 Arg Ser Val Met Ser Ala Ser Ser Trp Leu Val Thr Cys Gly Met Thr
 35 40 45
 Thr Gln Leu Arg Cys Arg Phe Phe Asp Gly Val Ile Ser Ala Leu Arg
 50 55 60
 Arg Val Thr His Tyr Trp Arg His Ile Met Gln Thr Leu Ser Ile Gln
 65 70 75 80
 His Gly Thr Leu Val Thr Met Asp Gln Tyr Arg Arg Val Leu Gly Asp
 85 90 95
 Ser Trp Val His Val Gln Asp Gly Arg Ile Val Ala Leu Gly Val His
 100 105 110
 Ala Glu Ser Val Pro Pro Pro Ala Asp Arg Val Ile Asp Ala Arg Gly
 115 120 125
 Lys Val Val Leu Pro Gly Phe Ile Asn Ala His Thr His Val Asn Gln
 130 135 140
 Ile Leu Leu Arg Gly Gly Pro Ser His Gly Arg Gln Phe Tyr Asp Trp
 145 150 155 160
 Leu Phe Asn Val Val Tyr Pro Gly Gln Lys Ala Met Arg Pro Glu Asp
 165 170 175
 Val Ala Val Ala Val Arg Leu Tyr Cys Ala Glu Ala Val Arg Ser Gly
 180 185 190
 Ile Thr Thr Ile Asn Glu Asn Ala Asp Ser Ala Ile Tyr Pro Gly Asn
 195 200 205
 Ile Glu Ala Ala Met Ala Val Tyr Gly Glu Val Gly Val Arg Val Val
 210 215 220
 Tyr Ala Arg Met Phe Phe Asp Arg Met Asp Gly Arg Ile Gln Gly Tyr
 225 230 235 240
 Val Asp Ala Leu Lys Ala Arg Ser Pro Gln Val Glu Leu Cys Ser Ile
 245 250 255
 Met Glu Glu Thr Ala Val Ala Lys Asp Arg Ile Thr Ala Leu Ser Asp
 260 265 270
 Gln Tyr His Gly Thr Ala Gly Gly Arg Ile Ser Val Trp Pro Ala Pro
 275 280 285
 Ala Thr Thr Thr Ala Val Thr Val Glu Gly Met Arg Trp Ala Gln Ala
 290 295 300
 Phe Ala Arg Asp Arg Ala Val Met Trp Thr Leu His Met Ala Glu Ser
 305 310 315 320
 Asp His Asp Glu Arg Ile His Gly Met Ser Pro Ala Asp Tyr Met Glu
 325 330 335

Cys Tyr Gly Leu Leu Asp Glu Arg Leu Gln Val Ala His Cys Val Tyr
 340 345 350

Phe Asp Arg Lys Asp Val Arg Leu Leu His Arg His Asn Val Lys Val
 355 360 365

Ala Ser Gln Val Val Ser Asn Ala Tyr Leu Gly Ser Gly Val Ala Pro
 370 375 380

Val Pro Glu Met Val Glu Arg Gly Met Ala Val Gly Ile Gly Thr Asp
 385 390 395 400

Asn Gly Asn Ser Asn Asp Ser Val Asn Met Ile Gly Asp Met Lys Phe
 405 410 415

Met Ala His Ile His Arg Ala Val His Arg Asp Ala Asp Val Leu Thr
 420 425 430

Pro Glu Lys Ile Leu Glu Met Ala Thr Ile Asp Gly Ala Arg Ser Leu
 435 440 445

Gly Met Asp His Glu Ile Gly Ser Ile Glu Thr Gly Lys Arg Ala Asp
 450 455 460

Leu Ile Leu Leu Asp Leu Arg His Pro Gln Thr Thr Pro His His His
 465 470 475 480

Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr Gly Asn Glu Val Asp Thr
 485 490 495

Val Leu Ile Asp Gly Asn Val Val Met Glu Asn Arg Arg Leu Ser Phe
 500 505 510

Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu Glu Glu Ala Gln Ser Arg
 515 520 525

Ala Thr Ala Ile Leu Gln Arg Ala Asn Met Val Ala Asn Pro Ala Trp
 530 535 540

Arg Ser Leu Glu Met Thr Pro Leu Leu His Pro Pro Pro Leu Glu Glu
 545 550 555 560

Ile Ala Ala Ile Leu Ala Arg Leu Gly Leu Gly Gly Gly His Asp Leu
 565 570 575

Asp Gly Tyr Arg Ile Ala Met Asn Ala Ala Leu Pro Ser Phe Ala Arg
 580 585 590

Val Glu Ser Leu Val Gly Glu Gly Arg Leu Arg Ala Pro Ala Ser Arg
 595 600 605

Arg Ser Glu Arg Pro Glu
 610

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGTATCGGG GAATTCTTGA GCGCGGCCAC AGCAGCCNTG ATCATGAAGG CGAGCATGGT	60
GACCTNGACG CCGTNTTTTN GTTNTTTTTT GTTGAAGTGC ACGCGAAAGG TTCCAGGTCG	120
GTGATGTCCG CGTCGTCGTG GTTGGTGACG TGCGGGATGA CCACCCAGNT GCGGTGCAGG	180
TTTTTCGATG GCATAATATC TGC GTTGCGA CGTGTAACAC ACTANTGGAG ACATATCATG	240
CAAACGCTCA GCATCCAGCA CCGTACCCTC GTCACGATGG ATCAGTACCG CAGAGTCCTT	300
GGGGATAGCT GGGTTCACGT GCAGGATGGA CGGATCGTCG CGCTCGGAGT GCACGCCGAG	360
TCGGTGCCTC CGCCAGCGGA TCGGGTGATC GATGCACGCG GCAAGGTCGT GTTACCCGGT	420
TTCATCAATG CCCACACCCA TGTGAACCAG ATCCTCCTGC GCGGAGGGCC CTCGCACGGG	480
CGTCAATTCT ATGACTGGCT GTTCAACGTT GTGTATCCGG GACAAAAGGC GATGAGACCG	540
GAGGA	545

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCTGCGCGGA GGGCCTCCGC ACGGGCGTCA ATTCTATGAC TGGCTGTTCA ACGTTGTGTA	60
TCCGGGACAA AAGGCGATGA GACCGGAGGA CGTAGCGGTG GCGGTGAGGT TGTATTGTGC	120
GGAAGCTGTG CGCAGCGGGA TTACGACGAT CAACGAAAAC GCCGATTCGG CCATCTACCC	180
AGGCAACATC GAGGCCGCGA TGGCGGTCTA TGGTGAGGTG GGTGTGAGGG TCGTCTACGC	240
CCGCATGTTT TTTGATCGGA TGGACGGGCG CATTCAAGGG TATGTGGACG CCTTGAAGGC	300
TCGCTCTCCC CAAGTCGAAC TGTGCTCGAT CATGGAGGAA ACGGCTGTGG CCAAAGATCG	360

GATCACAGCC CTGTCAGATC AGTATCATGG CACGGCAGGA GGTCCTATAT CAGTTTGGCC	420
CGCTCCTGCC ACTACCACGG CGGTGACATT TAAANGAATC CATGGGCCAA CCTCCCCCGT	480
GATCCGGCGG TAATGTGAC	499

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TNGCAGGTTG TGAGCATGCT ACTTCGGTTC AGGNGTGGCC CCCGTGCCAG AGATGGTGGA	60
GCGCGGCATG GCCGTGGGCA TTGGAACAGA TAACGGGAAT AGTAATGACT CCGTAAACAT	120
GATCGGAGAC ATGAAGTTTA TGGCCCATAT TCACCGCGCG GTGCATCGGG ATGCGGACGT	180
GCTGACCCCA GAGAAGATTN TTGAAATGGC GACGATCGAT GGGGCGCGTT TCGTTGGGGA	240
TGGACCACGA GATTGGTTCC ATCGAAACCG GCAAGCGCGC GGACCTTATC CTGCTTGACC	300
TGCGTCACCC TCAGACGACT CCTCACCATC ATTTGGCGGC CACGATCGTG TTTCAGGCTT	360

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGCCACGAT CGTGTTTCAG GCTTACGGCA ATGAGGTGGA CACTGTCCTG ATTGACGGAA	60
ACGTTGTGAT GGAGAACCGC CGCTTGAGCT TTCTTCCCCC TGAACGTGAG TTGGCGTTCC	120
TTGAGGAAGC GCAGAGCCGC GCCACAGCTA TTTTGCATCG GGCGAAACAT GGTGGCTAAC	180
CCAGCTTGGC GCAGCCTCTA GGAAATGACG CCGTTGCTGC ATCCGCCGCC CCTTGAGGAA	240
ATCGCTGCCA TCTTGGCGCG GCTCGGATTG GGGGGCGGAC ATGACCTTGA TGGATACAGA	300
ATTGCCATGA ATGCGGCACT TCCGTCCTTC GCTCGTGTGG AATCGTTGGT AGGTGAGGGT	360

CGACTGCGGG CGCCAGCTTC CCGAAGAGGT GAAAGCCCGA GGATCCTCTA GAGTCCGATT 420
 TTTCCGATGT CATCACCGGC GCG 443

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTGCGCGGA GGCCTCCGCA CGGGCGTCAA TTCTATGACT GGCTGTTCAA CGTTGTGTAT 60
 CCGGGACAAA AGGCGATGAG ACCGGAGGAC GTANCGGTGG CCGTGAGGTT GTATTGTGCG 120
 GAAGCTGTGC GCAGCGGGAT TACGACGATC AACGAAAACG CCGATTTCGGC CATCTACCCA 180
 GGCAACATCG AGGCCGCGAT GGCGGTCTAT GGTGAGGTGG GTGTGAGGGT CGTCTACGCC 240
 CGCATGTTCT TTGATCGGAT GGACGGGCGC ATTCAAGGGT ATGTGGACGC CTTGAAGGCT 300
 CGCTCTCCCC AAGTCGAACT GTGCTCGATC ATGGAGGAAA CGGCTGTGGC CAAAGATCGG 360
 ATCACANCCC TGTCAGATCA NTATCATGGC ACGGCANGAG GTCCTATATC ANTTTGGCCC 420
 GCTCCTGCCA CTACCACNGC GGTGACATTT NAANGAATTC CATNGGCACA ACCTTCCCCC 480
 GTGATCNGGC GGTAATGTNG ACCCA 505

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Pro His Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Leu Tyr Pro
 1 5 10 15
 Gly Gln Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu
 20 25 30
 Tyr Cys Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn
 35 40 45

Ala Asp Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val
50 55 60

Tyr Gly Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp
65 70 75 80

Arg Met Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg
85 90 95

Ser Pro Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala
100 105 110

Lys Asp Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly
115 120 125

Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr
130 135 140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser His Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Leu Tyr Pro
1 5 10 15

Gly Gln Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu
20 25 30

Tyr Cys Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn
35 40 45

Ala Asp Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val
50 55 60

Tyr Gly Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp
65 70 75 80

Arg Met Asp Gly Arg Ile Gln Gly Tyr Val Asp Thr Leu Lys Ala Arg
85 90 95

Ser Pro Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala
100 105 110

Lys Asp Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly
115 120 125

Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr
130 135 140

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro	His	Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro
1				5					10					15	
Gly	Gln	Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu
			20					25					30		
Tyr	Cys	Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn
		35					40					45			
Ala	Asp	Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val
	50					55				60					
Tyr	Gly	Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp
65					70				75					80	
Arg	Met	Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg
				85				90						95	
Ser	Pro	Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala
			100					105					110		
Lys	Asp	Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly
		115						120				125			
Gly	Arg	Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr
	130					135						140			

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser	His	Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Leu	Tyr	Pro
1				5					10					15	

Gly Gln Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu
 20 25 30
 Tyr Cys Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn
 35 40 45
 Asn Ala Asp Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala
 50 55 60
 Val Tyr Gly Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe
 65 70 75 80
 Asp Arg Met Asp Gly Arg Ile Gln Gly Tyr Val Asp Thr Leu Lys Ala
 85 90 95
 Arg Ser Pro Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val
 100 105 110
 Ala Lys Asp Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala
 115 120 125
 Gly Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val
 130 135 140
 Thr
 145

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser His Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro
 1 5 10 15
 Gly Gln Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu
 20 25 30
 Tyr Cys Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn
 35 40 45
 Ala Asp Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val
 50 55 60
 Tyr Gly Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp
 65 70 75 80
 Arg Met Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg
 85 90 95

Ser Pro Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala
100 105 110

Gly Arg Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr
130 135 140

TGGTGGAGCG	CGGCATGGCC	GTGGGCATTG	GAACAGATAA	CGGGAATAGT	AATGACTCCG	1140
TAAACATGAT	CGGAGACATG	AAGTTTATGG	CCCATATTCA	CCGCGCGGTG	CATCGGGATG	1200
CGGACGTGCT	GACCCAGAG	AAGATTCTTG	AAATGGCGAC	GATCGATGGG	GCGCGTTCGT	1260
TGGGGATGGA	CCACGAGATT	GGTTCCATCG	AAACCGGCAA	GCGCGCGGAC	CTTATCCTGC	1320
TTGACCTGCG	TCACCCTCAG	ACGACTCCTC	ACCATCATTT	GGCGGCCACG	ATCGTGTTTC	1380
AGGCTTACGG	CAATGAAGTG	GACACTGTCC	TGATTGACGG	AAACGTTGTG	ATGGAGAACC	1440
GCTGCTTGAG	CTTTCTTCCC	CCTGAACGTG	AGTTGGCGTT	CCTTGAGGGA	GCGCAGAGCC	1500
GCGCCACAGC	TATTTTGAG	CGGGCGAACA	TGGTGGCTAA	CCCAGCTTGG	GCGAGCCTCT	1560
AGGAAATGAC	GCCGTTGCTG	CATCCGCCGC	CCCTTGAGGA	AATCGCTGCC	ATCTTGCGCG	1620
GGCTCGGATT	GGG					1633

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGTGGTTGG	TGACGTGCGG	GATGACCACC	CAGTCGCGGT	GCAGGTTTTT	CGATGGCATA	60
ATATCTGCGT	TGCGACGTGT	AACACACTAT	TGGAGACATA	TCATGCAAAC	GCTCAGCATC	120
CAGCACGGTA	CCCTCGTCAC	GATGGATCAG	TACCGCAGAG	TCCTTGGGGA	TAGCTGGGTT	180
CACGTGCAGG	ATGGACGGAT	CGTCGCGCTC	GGAGTGCACG	CCGAGTCGGT	GCCTCCGCCA	240
GCGGATCGGG	TGATCGATGC	ACGCGGCAAG	GTCGTGTTAC	CCGTTTTCAT	CAATGCCAC	300
ACCCATGTGA	ACCAGATCCT	CCTGCGCGGA	GGGCCCTCGC	ACGGGCGTCA	ATTCTATGAC	360
TGGCTGTTCA	ACGTTGTGTA	TCCGGGACAA	AAGGCGATGA	GACCGGAGGA	CGTAGCGGTG	420
GCGGTGAGGT	TGTATTGTGC	GGAAGCTGTG	CGCAGCGGGA	TTACGACGAT	CAACGAAAAC	480
GCCGATTTCG	CCATCTACCC	AGGCAACATC	GAGGCCGCGA	TGGCGGTCTA	TGGTGAGGTG	540
GGTGTGAGGG	TCGTCTACGC	CCGCATGTTT	TTTGATCGGA	TGGACGGGCG	CATTCAAGGG	600
TATGTGGACG	CCTTGAAGGC	TCGCTCTCCC	CAAGTCGAAC	TGTGCTCGAT	CATGGAGGAA	660
ACGGCTGTGG	CCAAAGATCG	GATCACAGCC	CTGTCAGATC	AGTATCATGG	CACGGCAGGA	720
GGTCGTATAT	CAGTTTGGCC	CGCTCCTGCC	ACTACCACGG	CGGTGACAGT	TGAAGGAATG	780

CGATGGGCAC AAGCCTTCGC CCGTGATCGG GCGGTAATGT GGACGCTTCA CATGGCGGAG	840
AGCGATCATG ATGAGCGGAT TCATGGGATG AGTCCC GCCG AGTACATGGA GTGTCACGGA	900
CTCTTGGATG AGCGTCTGCA GGTGCGCAT TGCGTG TACT TTGACCGGAA GGATGTTCCG	960
CTGCTGCACC GCCACAATGT GAAGGTCGCG TCGCAGGTTG TGAGCAATGC CTACCTCGGC	1020
TCAGGGGTGG CCCCCGTGCC AGAGATGGTG GAGCGCGGCA TGGCCATGGG CATTGGAACA	1080
GATAACGGGA ATAGTAATGA CTCCGTAAAC ATGATCGGAG ACATGAAGTT TATGGCCCAT	1140
ATTCACCGCG CGGTGCATCG GGATGCGGAC GTGCTGACCC CAGAGAAGAT TCTTGAAATG	1200
GCGACGATCG ATGGGGCGCG TTCGTTGGGA ATGGACCACG AGATTGGTTC CATCGAAACC	1260
GGCAAGCGCG CGGACCTTAT CCTGCTTGAC CTGCGTCACC CTCAGACGAC TCCTCACCAT	1320
CATTTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC TGTCTGATT	1380
GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA ACGTGAGTTG	1440
GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC GAACATGGTG	1500
GCTAACCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC GCCGCCCTT	1560
GAGGAAATCG CTGCCATCTT GGCGCGGCTC GGATTGGG	1598

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACGTGCGGGA TGACCACCCA GTTGCGGTGC AGGTTTTTCG ATGGCGTAAT ATCTGCGTTG	60
CGACGTGTAA CAACTATTG GAGACATATC ATGCAAACGC TCAGCATCCA GCACGGTACC	120
CTCGTCACGA TGGATCAGTA CCGCAGAGTC CTTGGGGATA GCTGGGTTCA CGTGCAGGAT	180
GGACGGATCG TCGCGCTCGG AGTGACGCC GAGTCGGTGC CTCCGCCAGC GGATCGGGTG	240
ATCGATGCAC GCGCAAGGT CGTGTTACCC GGTTCATCA ATGCCACAC CCATGTGAAC	300
CAGATCCTCC TGCGCGGAGG GCCCTCGCAC GGGCGTCAAT TCTATGACTG GCTGTTCAAC	360
GTTGTGTATC CGGGACAAA GCGATGAGA CCTGAGGACG TAGCGGTGGC GGTGAGGTTG	420
TATTGTGCGG AAGCTGTGCG CAGCGGGATT ACGACGATCA ACGAAAACGC CGATTGCGCC	480
ATCTACCCAG GCAACATCGA GGCCGCGATG GCGGTCTATG GTGAGGTGGG TGTGAGGGTC	540

GTCTACGCCC GCATGTTCTT TGATCGGATG GACGGGCGCA TTCAAGGGTA TGTGGACGCC	600
TTGAAGGCTC GCTCTCCCCA AGTCGAACTG TGCTCGATCA TGGAGGAAAC GGCTGTGGCC	660
AAAGATCGGA TCACAGCCCT GTCAGATCAG TATCATGGCA CGGCAGGAGG TCGTATATCA	720
GTTTGGCCCG CTCCTGCCAC TACCACGGCG GTGACAGTTG AAGGAATGCG ATGGGCACAA	780
GCCTTCGCCC GTGATCGGGC GGTAATGTGG ACGCTTCACA TGGCGGAGAG CGATCATGAT	840
GAGCGGATTC ATGGGATGAG TCCCGCCGAG TACATGGAGT GTTACGGACT CTTGGATGAG	900
CGTCTGCAGG TCGCGCATTG CGTGTACTTT GACCGGAAGG ATGTTCGGCT GCTGCACCGC	960
CACAATGTGA AGGTCGCGTC GCAGGTTGTG AGCAATGCCT ACCTCGGCTC AGGGGTGGCC	1020
CCCGTGCCAG AGATGGTGGA GCGCGGCATG GCCGTGGGCA TTGGAACAGA TAACGGGAAT	1080
AGTAATGACT CCGTAAACAT GATCGGAGAC ATGAAGTTTA TGGCCCATAT TCACCGCGCG	1140
GTGCATCGGG ATGCGGACGT GCTGACCCCA GAGAAGATTC TTGAAATGGC GACAATCGAT	1200
GGGGCGCGTT CGTTGGGAAT GGACCACGAG ATTGGTTCCA TCGAAACCGG CAAGCGCGCG	1260
GACCTTATCC TGCTTGACCT GCGTCACCTT CAGACGACTC CTCACCATCA TTTGGCGGCC	1320
ACGATCGTGT TTCAGGCTTA CGGCAATGAG GTGGACACTG TCCTGATTGA CGGAAACGTT	1380
GTGATGGAGA ACCGCCGCTT GAGCTTTCTT CCCCCTGAAC GTGAGTTGGC GTTCCTTGAG	1440
GAAGCGCAGA GCCGCGCCAC AGCTATTTTG CAGCGGGCGA ACATGGTGGC TAACCCAGCT	1500
TGGCGCAGCC TCTAGGAAAT GACGCCGTTG CTGCATCCGC TGCCCCTTGA GGAAATCGCT	1560
GCCATCTTGG CGCGGCTCGG ATTGGG	1586

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGGTTGGT GACGTGGGGG ATGACCACCC AGTCGCGGTG CAGGTTTTTC GATGGCATAA	60
TATCTGCGTT GCGACGTGTA ACACACTATT GGAGACATAT CATGCAAACG CTCAGCATCC	120
AGCACGGTAC CCTCGTCACG ATGGATCAGT ACCGCAGAGT CCTTGGGGAT AGCTGGGTTC	180
ACGTGCAGGA TGGACGGATC GTCGCGCTCG GAGTGCACGC CGAGTCGGTG CCTCCGCCAG	240
CGGATCAGGT GATCGATGCA CGCGGCAAGG TCGTGTTACC CGGTTTCATC AATGCCACAA	300

CCCATGTGAA CCAGATCCTC CTGCGCGGAG GGCCCTCGCA CGGGCGTCAA TTCCATGACT	360
GGCTGTTCAA CGTTGTGTAT CCGGGACAAA AGGCGATGAG ACCGGAGGAC GTAGCGGTGG	420
CGGTGAGGTT GTATTGTGCA GAAGCTGTGC GCAGCGGGAT TACGACGATT AACGAAAACG	480
CCGATTCGGC CATCTACCCA GGCAACATCG AGGCCGCGAT GGCGGTCTAT GGTGAGGTGG	540
GTGTGAGGGT CGTCTACGCC CGCATGTTCT TTGATCGGAT GGACGGGCGC ATTCAAGGGT	600
ATGTGGACGC CTTGAAGGCT CGCTCTCCCC AAGTCGAACT GTGCTCGATC ATGGAGGAAA	660
CGGCTGTGGC CAAAGATCGG ATCACAGCCC TGTCAGATCA GTATCATGGC ACGGCAGGAG	720
GTCGTATATC AGTTTGGCCC GCTCCTGCCA CTACCACGGC GGTGACAGTT GAAGGAATGC	780
GATGGGCACA AGCCTTCGCC CGTGATCGGG CGGTAATGTG GACGCTTCAC ATGGCGGAGA	840
GCGATCATGA TGGGCGGATT CATGGGATGA GTCCCGCCGA GTACATGGAG TGTTACGGAC	900
TCTTGATGA GCGTCTGCAG GTCGCGCATT GCGTGTACTT TGACCGGAAG GATGTTCCGGC	960
TGCTGCACCG CCACAATGTG AAGGTCGCGT CGCAGGTTGT GAGCAATGCC TACCTCGGCT	1020
CAGGGGTGGC CCCCCTGCCA GAGATGGTGG AGCGCGGCAT GGCCGTGGGC ATTGGAACAG	1080
ATAACGGGAA TAGTAATGAC TCCGTAAACA TGATCGGAGA CATGAAGTTT ATGGCCCATA	1140
TTCACCGCGC GGTGCATCGG GATGCGGACG TGCTGACCCC AGAGAAGATT CTTGAAATGG	1200
CAACGATCGA TGGGGCGCGT TCGTTGGGAA TGGACCACGA GATTGGTTCC ATCGAAACCG	1260
GCAAGCGCGC GGACCTTATC CTGCTTGACC TCGTCACCC TCAGACGACT CCTCACCATC	1320
ATTTGGCGGC CACGATCGTG TTTCAGGCTT ACGGCAATGA GGTGGACACT GTCCTGATTG	1380
ACGGAAACGT TGTGATGGAG AACCGCCGCT TGAGCTTTCT TCCCCCTGAA CGTGAGTTGG	1440
CGTTCCTTGA GGAAGCGCAG AGCCGCGCCA CAGCTATTTT GCAGCGGGCG AACATGGTGG	1500
CTAACCCAGC TTGGCGCAGC CTCTAGGAAA TGACGCCGTT GCTGCATCCG CCGCCCCTTG	1560
AGGAAATCGC TGCCATCTTG GCGCGGCTCG GATTGGG	1597

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGACCTTGA CGCCGCTCTT TTCGTTCTCT TTGTTGAACT GCACGCGAAT GGCTTCCAGT	60
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TCGATGATGT	CCGCGTCGTC	GTGGTTGGTG	ACGTGCGGGA	TGACCACCCA	GTCGCGGTGC	120
AGGTTTTTCG	ATGGCATAAT	ATCTGCGTTG	CGACGTGTAA	CACACTATTG	GAGACATATC	180
ATGCAAACGC	TCAGCATCCA	GCACGGTACC	CTCGTCACGA	TGGATCAGTA	CCGCAGAGTC	240
CTTGGGGATA	GCTGGGTTCA	CGTGCAGGAT	GGACGGATCG	TCGCGCTCGG	AGTGCACGCC	300
GAGTCGGTGC	CTCCGCCAGC	GGATCGGGTG	ATTGATGCAC	GCGGCAAGGT	CGTGTTACCC	360
GGTTTCATCA	ATGCCCACAC	CCATGTGAAC	CAGATCCTCC	TGCGCGGAGG	CCTCGCACGG	420
GCGTCAATTC	TATGACTGGC	TGTTCAACGT	TGTGTATCCG	GGACAAAAGG	CGATGAGACC	480
GGAGGACGTA	GCGGTGGCGG	TGAGGTTGTA	TTGTGCGGAA	GCTGTGCGCA	GCGGGATTAC	540
GACGATCAAC	GAAAACGCCG	ATTCGGCCAT	CTACCCAGGC	AACATCGAGG	CCGCGATGGC	600
GGTCTATGGT	GAGGTGGGTG	TGAGGGTCGT	CTACGCCCCG	ATGTTCTTTG	ATCGGATGGA	660
CAGGCGCATT	CAAGGGTATG	TGGACGCCTT	GAAGGCTCGC	TCTCCCCAAG	TCGAACTGTG	720
CTCGATCATG	GAGGAAACGG	CTGTGGCCAA	AGATCGGATC	ACAGCCCTGT	CAGATCAGTA	780
TCATGGCACG	GCAGGAGGTC	GTATATCAGT	TTGGCCCGCT	CCTGCCACTA	CCACGGCGGT	840
GACAGTTGAA	GGAATGCGAT	GGGCACAAGC	CTTCGCCCCG	GATCGGGCGG	TAATGTGGAC	900
GCTTCACATG	GCGGAGAGCG	ATCATGATGA	GCGGATTCAT	GGGATGAGTC	CCGCCGAGTA	960
CATGGAGTGT	TACGGACTCT	TGGATGAGCG	TCTGCAGGTC	GCGCATTGCG	TGTACTTTGA	1020
CCGGAAGGAT	ATTCGGCTGC	TGCACCGCCA	CAATGTGAAG	GTCGCGTCGC	AGGCTGTGAG	1080
CAATGCCTAC	CTCGGCTCAG	GGGTGGCCCC	CGTGCCAGAG	ATGGTGGAGC	GCGGCATGGC	1140
CGTGGGCATT	GGAACAGATA	ACGGGAATAG	TAATGACTCC	GTAAACATGA	TCGGAGACAT	1200
GAAGTTTATG	GCCCATATTC	ACCGCGCGGT	GCATCGGGAT	GCGGACGTGC	TGACCCAGAG	1260
GAAGATTCTT	GAAATGGCGA	CGATCGATGG	GGCGCGTTTC	TTGGGAATGG	ACCACGAGAT	1320
TGGTTCCATC	GAAACCGGCA	AGCGCGCGGA	CCTTATCCTG	CTTGACCTGC	GTCACCCTCA	1380
GACGACTCCT	CACCATCATT	TGGCGGCCAC	GATCGTGTTT	CAGGCTTACG	GCAATGAGGT	1440
GGACACTGTC	CTGATTGACG	GAAACGTTGT	GATGGAGAAC	CGCCGCTTGA	GCTTTCTTCC	1500
CCCTGAACGT	GAGTTGGCGT	TCCTTGAGGA	AGCGCAGAGC	CGCGCCACAG	CTATTTTGCA	1560
GCGGGCGAAC	ATGGTGGCCA	ACCCAGCTTG	GCGCAGCCTC	TAGGAAATGA	CGCCGTTGCT	1620
GCATCCGCCG	CCCCTTGAGG	AAATCGCTGC	CATCTTGGCG	CAGCTCGGAT	TGGG	1674

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln
1          5          10          15
Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg
20          25          30
Ile Val Ala Leu Gly Val His Ala Lys Ser Val Pro Pro Pro Ala Asp
35          40          45
Arg Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn
50          55          60
Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
65          70          75          80
Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
85          90          95
Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
100         105         110
Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
115         120         125
Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
130         135         140
Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
145         150         155         160
Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
165         170         175
Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
180         185         190
Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
195         200         205
Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
210         215         220
Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
225         230         235         240
```


Thr Leu His Met Ala Glu Ser Asp His Asp Gly Arg Ile His Gly Met
 245 250 255
 Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270
 Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285
 His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300
 Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320
 Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Val Asn
 325 330 335
 Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350
 Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
 355 360 365
 Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
 370 375 380
 Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Pro
 385 390 395 400
 Gln Thr Thr Pro His His His Leu Ala Ala Thr Ile Val Phe Gln Ala
 405 410 415
 Tyr Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met
 420 425 430
 Glu Asn Arg Cys Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe
 435 440 445
 Leu Glu Gly Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn
 450 455 460
 Met Val Ala Asn Pro Ala Trp Arg Ser Leu Glu Met Thr Pro Leu Leu
 465 470 475 480
 His Pro Pro Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Arg Leu Gly
 485 490 495

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln	
1				5					10					15		
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg	
			20					25					30			
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp	
		35					40					45				
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn	
	50					55					60					
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His	
65					70					75					80	
Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	Gly	Gln	
			85						90					95		
Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys	
			100					105						110		
Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp	
		115					120						125			
Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly	
	130					135					140					
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met	
145					150					155					160	
Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro	
			165						170					175		
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp	
		180						185					190			
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	
		195					200						205			
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	
	210					215					220					
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	
225					230					235					240	
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met	
			245						250					255		
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	His	Gly	Leu	Leu	Asp	Glu	Arg	Leu	
		260						265					270			
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu	
		275					280						285			
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr	
	290					295					300					
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	
305					310					315					320	

Ala	Met	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	325	330	335	
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His	340	345	350	
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	355	360	365	
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	370	375	380	
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro	385	390	395	400
Gln	Thr	Thr	Pro	His	His	His	Leu	Ala	Ala	Thr	Ile	Val	Phe	Gln	Ala	405	410	415	
Tyr	Gly	Asn	Glu	Val	Asp	Thr	Val	Leu	Ile	Asp	Gly	Asn	Val	Val	Met	420	425	430	
Glu	Asn	Arg	Arg	Leu	Ser	Phe	Leu	Pro	Pro	Glu	Arg	Glu	Leu	Ala	Phe	435	440	445	
Leu	Glu	Glu	Ala	Gln	Ser	Arg	Ala	Thr	Ala	Ile	Leu	Gln	Arg	Ala	Asn	450	455	460	
Met	Val	Ala	Asn	Pro	Ala	Trp	Arg	Ser	Leu	Glu	Met	Thr	Pro	Leu	Leu	465	470	475	480
His	Pro	Pro	Pro	Leu	Glu	Glu	Ile	Ala	Ala	Ile	Leu	Ala	Arg	Leu	Gly	485	490	495	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln	1	5	10	15
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg	20	25	30	
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp	35	40	45	
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn	50	55	60	

Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His
 65 70 75 80
 Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95
 Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110
 Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125
 Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140
 Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160
 Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175
 Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190
 Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205
 Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220
 Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240
 Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255
 Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270
 Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285
 His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300
 Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320
 Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Val Asn
 325 330 335
 Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350
 Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
 355 360 365
 Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
 370 375 380
 Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Pro

385		390		395		400
Gln Thr Thr Pro His His His Leu Ala Ala Thr Ile Val Phe Gln Ala						
		405		410		415
Tyr Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met						
		420		425		430
Glu Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe						
		435		440		445
Leu Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn						
		450		455		460
Met Val Ala Asn Pro Ala Trp Arg Ser Leu Glu Met Thr Pro Leu Leu						
		465		470		475
				475		480
His Pro Leu Pro Leu Glu Glu Ile Ala Ala Ile Leu Ala Arg Leu Gly						
		485		490		495

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Gln Thr Leu Ser Ile Gln His Gly Thr Leu Val Thr Met Asp Gln															
1				5				10					15		
Tyr Arg Arg Val Leu Gly Asp Ser Trp Val His Val Gln Asp Gly Arg															
			20				25					30			
Ile Val Ala Leu Gly Val His Ala Glu Ser Val Pro Pro Pro Ala Asp															
		35				40				45					
Gln Val Ile Asp Ala Arg Gly Lys Val Val Leu Pro Gly Phe Ile Asn															
		50				55				60					
Ala His Thr His Val Asn Gln Ile Leu Leu Arg Gly Gly Pro Ser His															
		65			70			75					80		
Gly Arg Gln Phe His Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln															
			85				90						95		
Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys															
		100				105						110			
Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp															
		115				120						125			

Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140

Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160

Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175

Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190

Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205

Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220

Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240

Thr Leu His Met Ala Glu Ser Asp His Asp Gly Arg Ile His Gly Met
 245 250 255

Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270

Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285

His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300

Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320

Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Val Asn
 325 330 335

Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
 340 345 350

Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
 355 360 365

Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
 370 375 380

Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Pro
 385 390 395 400

Gln Thr Thr Pro His His His Leu Ala Ala Thr Ile Val Phe Gln Ala
 405 410 415

Tyr Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met
 420 425 430

Glu Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe
 435 440 445

Leu	Glu	Glu	Ala	Gln	Ser	Arg	Ala	Thr	Ala	Ile	Leu	Gln	Arg	Ala	Asn
450						455					460				
Met	Val	Ala	Asn	Pro	Ala	Trp	Arg	Ser	Leu	Glu	Met	Thr	Pro	Leu	Leu
465					470					475					480
His	Pro	Pro	Pro	Leu	Glu	Glu	Ile	Ala	Ala	Ile	Leu	Ala	Arg	Leu	Gly
				485					490						495

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 496 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln
1				5				10					15		
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg
			20				25					30			
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp
	35					40					45				
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn
	50				55					60					
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His
65				70				75					80		
Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	Gly	Gln
		85					90					95			
Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys
		100					105					110			
Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp
	115					120					125				
Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly
	130				135					140					
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met
145				150				155						160	
Asp	Arg	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro
			165				170						175		
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp
			180				185						190		

Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg	195	200	205
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu	210	215	220
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp	225	230	235
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met	245	250	255
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu	260	265	270
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Ile	Arg	Leu	Leu	275	280	285
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Ala	Val	Ser	Asn	Ala	Tyr	290	295	300
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met	305	310	315
Ala	Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Val	Asn	325	330	335
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His	340	345	350
Arg	Asp	Ala	Asp	Val	Leu	Thr	Pro	Glu	Lys	Ile	Leu	Glu	Met	Ala	Thr	355	360	365
Ile	Asp	Gly	Ala	Arg	Ser	Leu	Gly	Met	Asp	His	Glu	Ile	Gly	Ser	Ile	370	375	380
Glu	Thr	Gly	Lys	Arg	Ala	Asp	Leu	Ile	Leu	Leu	Asp	Leu	Arg	His	Pro	385	390	395
Gln	Thr	Thr	Pro	His	His	His	Leu	Ala	Ala	Thr	Ile	Val	Phe	Gln	Ala	405	410	415
Tyr	Gly	Asn	Glu	Val	Asp	Thr	Val	Leu	Ile	Asp	Gly	Asn	Val	Val	Met	420	425	430
Glu	Asn	Arg	Arg	Leu	Ser	Phe	Leu	Pro	Pro	Glu	Arg	Glu	Leu	Ala	Phe	435	440	445
Leu	Glu	Glu	Ala	Gln	Ser	Arg	Ala	Thr	Ala	Ile	Leu	Gln	Arg	Ala	Asn	450	455	460
Met	Val	Ala	Asn	Pro	Ala	Trp	Arg	Ser	Leu	Glu	Met	Thr	Pro	Leu	Leu	465	470	475
His	Pro	Pro	Pro	Leu	Glu	Glu	Ile	Ala	Ala	Ile	Leu	Ala	Gln	Leu	Gly	485	490	495